

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2022-04-23, 09:03 based on data in: `/home/khoidnyds/RNAseq_old/3.cutadapt`

Welcome!

Not sure where to start?

Watch a tutorial video

(6:06)

don't show again

General Statistics

Copy table

Showing 6/6 rows.

Sample Name	% BP Trimmed
SRR14689338_mixed	0.0%
SRR14689339_mixed	0.0%
SRR14689340_lymphoblastic	0.0%
SRR14689341_lymphoblastic	0.0%
SRR14689344_myeloid	0.0%
SRR14689345_myeloid	0.0%

Cutadapt

[Cutadapt](#) is a tool to find and remove adapter sequences, primers, poly-A tails and other types of unwanted sequence from your high-throughput sequencing reads. *DOI: 10.14806/ej.17.1.200.*

Filtered Reads

This plot shows the number of reads (SE) / pairs (PE) removed by Cutadapt.

